

# Complete Genome Sequence of the Aerobic Marine Methanotroph *Methylomonas methanica* MC09

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***Methylomonas methanica* MC09 is a mesophilic, halotolerant, aerobic, methanotrophic member of the Gammaproteobacteria, isolated from coastal seawater. Here we present the complete genome sequence of this strain, the first available from an aerobic marine methanotroph.**

*Methylomonas methanica* (11, 21) is one of four recognized species within the genus *Methylomonas* in the Gammaproteobacteria, which includes *M. aurantiaca* (3, 12), *M. fodinarum* (3, 12), and *M. scandinavica* (13, 14). Several other *Methylomonas* species without validly published names have also been described, including “*M. clara*” (8) and “*M. rubra*” (18). All members of the genus use methane as the sole carbon and energy source. The majority of known strains were obtained from terrestrial environments; however, *M. methanica* MC09 was isolated from a methane enrichment culture inoculated with seawater obtained from the coast of Penarth, United Kingdom (lat 51.43, long –3.17) (M. Cunliffe and J. C. Murrell, unpublished data). *Methylomonas* spp. are prevalent in various marine and estuarine environments (5, 9, 16, 19, 20). The complete genome sequence of *M. methanica* MC09 is the first available for a marine methanotroph, providing insights into methane cycling in marine environments.

The genome (5.05 Mbp) of *M. methanica* MC09 was assembled using VELVET (22) and Newbler from an Illumina GAii (2) shotgun library (74,177,086 reads; 2.67 Gbp) and 454 Titanium (15) standard (215,708 reads) and paired-end (154 Mbp) libraries representing 24.3× coverage. Gaps were closed by PCR and Bubble PCR primer walks (350 reactions and 1 shatter library) using Consed (7). The genome is a single circular replicon with 4,494 candidate protein-encoding genes, as predicted by Prodigal (10) and GenePrimp (17). The mean GC content of the sequence was 51.3 mol%.

Synthetic pathways for tRNAs of all 20 structural amino acids were accounted for, along with a single rRNA operon. Three terminal oxidases were predicted: *aa*<sub>3</sub>, *o*-quinol, and *bd*-quinol.

All genes for the 2-keto-3-deoxy-6-phosphogluconate (KDPG) aldolase variant of the ribulose monophosphate (RuMP) pathway of formaldehyde fixation were predicted, consistent with experimental data for *Methylomonas* spp. (1). All genes of the pentose phosphate and Embden-Meyerhof-Parnas pathways were predicted. Genes for all enzymes of Krebs' cycle, with the exception of fumarase, were predicted. Genes for RubisCO were not found. The *mxsFJGIRSACKLDEK* cluster encoding methanol dehydrogenase was predicted, along with the cluster *pqqBCDE* for biosynthesis of the cofactor pyrroloquinoline quinone. Both particulate (*pmoCAB*) and soluble (*mmoXYBZDCGR*) methane monooxygenases were predicted. Acetate kinase and acetyl coenzyme A synthase were predicted, potentially allowing C<sub>2</sub>-compound assimilation.

All genes required for dinitrogen fixation were predicted, as were those for nitrate/nitrite transport (*nasFED*), ammonification (*nasCA*, *nasB*, and *nirBD*), direct ammonium uptake (*amtB*), and nitrogen assimilation (*glnA*, *gltB*, and *ald*). Urea metabolism genes were predicted (carbamoyl phosphate synthase, *carA* and *carB*; urease, *ureABC*); however, neither a complete urea cycle (lacking the arginase gene) nor functional urease (lacking accessory genes) is present. Genes for nitrite reduction (*nirS*) and nitric oxide reduction (*norB*) were predicted. A gene encoding cytochrome P460 was predicted, indicating a potential for hydroxylamine detoxification (4, 6).

The information provided in the complete genome sequence of *M. methanica* MC09 will enable further studies of the metabolism of this and other methanotrophic bacteria. These data also provide the first overview of the metabolic diversity of a marine methanotroph.

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**Nucleotide sequence accession number.** The nucleotide sequence of the genome has been deposited in DDBJ/EMBL/GenBank under accession no. CP002738.

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